



## SEQUENCE LISTING

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<120> Lipopolysaccharide alpha-2,3 Sialyltransferase of  
Campylobacter jejuni and Its Uses

<130> 019633-000912US

<140> US 10/799,016  
<141> 2004-03-11

<150> US 60/078,891  
<151> 1998-03-20

<150> US 09/272,960  
<151> 1999-03-18

<150> US 10/058,636  
<151> 2002-01-29

<160> 8

<170> PatentIn Ver. 2.0

<210> 1  
<211> 1293  
<212> DNA  
<213> Campylobacter jejuni

<220>  
<221> CDS  
<222> (1)..(1293)  
<223> Campylobacter jejuni OH4384 cst-I gene  
alpha2,3-sialyltransferase

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Met Thr Arg Thr Arg Met Glu Asn Glu Leu Ile Val Ser Lys Asn Met  
1 5 10 15  
caa aat ata atc ata gca gga aat gga cct agc cta aaa aat att aat 96  
Gln Asn Ile Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Asn Ile Asn  
20 25 30  
tat aaa aga ctg cct aga gaa tat gat gtt ttt agg tgt aac cag ttt 144  
Tyr Lys Arg Leu Pro Arg Glu Tyr Asp Val Phe Arg Cys Asn Gln Phe  
35 40 45  
tat ttt gaa gat aag tat tat tta gga aaa aag att aaa gca gta ttt 192  
Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Ile Lys Ala Val Phe  
50 55 60  
ttt aat cct ggt gtc ttt tta caa cag tat cac act gca aaa caa ctt 240  
Phe Asn Pro Gly Val Phe Leu Gln Gln Tyr His Thr Ala Lys Gln Leu  
65 70 75 80

ata cta aaa aat gag tat gaa ata aaa aat att ttt tgc tct aca ttt	288
Ile Leu Lys Asn Glu Tyr Glu Ile Lys Asn Ile Phe Cys Ser Thr Phe	
85 90 95	
aat tta cct ttt att gaa agc aat gat ttt tta cat caa ttt tat aat	336
Asn Leu Pro Phe Ile Glu Ser Asn Asp Phe Leu His Gln Phe Tyr Asn	
100 105 110	
ttt ttc ccc gat gca aaa ctt ggc tat gaa gtt att gaa aac ctt aaa	384
Phe Phe Pro Asp Ala Lys Leu Gly Tyr Glu Val Ile Glu Asn Leu Lys	
115 120 125	
gaa ttt tat gct tat ata aaa tac aat gaa att tat ttc aat aaa aga	432
Glu Phe Tyr Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr Phe Asn Lys Arg	
130 135 140	
att act tcg ggc gtc tat atg tgt gca att gct att gca tta gga tat	480
Ile Thr Ser Gly Val Tyr Met Cys Ala Ile Ala Ile Ala Leu Gly Tyr	
145 150 155 160	
aaa acc atc tat tta tgt ggc att gat ttt tat gaa gga gat gtt att	528
Lys Thr Ile Tyr Leu Cys Gly Ile Asp Phe Tyr Glu Gly Asp Val Ile	
165 170 175	
tat cct ttt gaa gct atg agt aca aat ata aaa aca atc ttt cct gga	576
Tyr Pro Phe Glu Ala Met Ser Thr Asn Ile Lys Thr Ile Phe Pro Gly	
180 185 190	
ata aaa gat ttc aaa cct tca aat tgt cat tct aag gaa tac gat ata	624
Ile Lys Asp Phe Lys Pro Ser Asn Cys His Ser Lys Glu Tyr Asp Ile	
195 200 205	
gaa gca tta aaa ttg tta aaa tca ata tac aaa gtt aat atc tac gca	672
Glu Ala Leu Lys Leu Leu Lys Ser Ile Tyr Lys Val Asn Ile Tyr Ala	
210 215 220	
ttg tgt gat gat tct att ttg gca aat cat ttt cct tta tca att aat	720
Leu Cys Asp Asp Ser Ile Leu Ala Asn His Phe Pro Leu Ser Ile Asn	
225 230 235 240	
att aat aac aat ttc act tta gaa aat aag cat aat aat tct ata aat	768
Ile Asn Asn Asn Phe Thr Leu Glu Asn Lys His Asn Asn Ser Ile Asn	
245 250 255	
gat att tta ttg act gat aat act cct ggc gta agt ttt tat aaa aat	816
Asp Ile Leu Leu Thr Asp Asn Thr Pro Gly Val Ser Phe Tyr Lys Asn	
260 265 270	
caa ctt aaa gct gat aat aaa att atg ctt aat ttt tat aat att ctt	864
Gln Leu Lys Ala Asp Asn Lys Ile Met Leu Asn Phe Tyr Asn Ile Leu	
275 280 285	
cat tct aaa gat aat tta att aaa ttt tta aac aaa gaa att gcg gta	912
His Ser Lys Asp Asn Leu Ile Lys Phe Leu Asn Lys Glu Ile Ala Val	
290 295 300	
tta aaa aaa caa acc act caa cga gct aaa gca aga atc caa aac cat	960
Leu Lys Lys Gln Thr Thr Gln Arg Ala Lys Ala Arg Ile Gln Asn His	
305 310 315 320	

cta tcc tat aaa cta gga caa gct ttg att ata aat tct aaa agt gta	1008
Leu Ser Tyr Lys Leu Gly Gln Ala Leu Ile Ile Asn Ser Lys Ser Val	
325 330 335	
tta ggt ttt tta tct tta cct ttt ata ata tta agt atc gtt att tca	1056
Leu Gly Phe Leu Ser Leu Pro Phe Ile Ile Leu Ser Ile Val Ile Ser	
340 345 350	
cat aaa caa gaa caa aag gct tat aaa ttt aaa gta aag aaa aat cca	1104
His Lys Gln Glu Gln Lys Ala Tyr Lys Phe Lys Val Lys Lys Asn Pro	
355 360 365	
aat tta gct tta cct cct tta gaa act tat cct gat tat aat gaa gct	1152
Asn Leu Ala Leu Pro Pro Leu Glu Thr Tyr Pro Asp Tyr Asn Glu Ala	
370 375 380	
tta aaa gaa aaa gaa tgt ttt act tat aaa tta gga gaa gaa ttt ata	1200
Leu Lys Glu Lys Glu Cys Phe Thr Tyr Lys Leu Gly Glu Glu Phe Ile	
385 390 395 400	
aaa gct ggt aag aat tgg tat ggg gag ggg tat atc aaa ttt ata ttc	1248
Lys Ala Gly Lys Asn Trp Tyr Gly Glu Gly Tyr Ile Lys Phe Ile Phe	
405 410 415	
aaa gat gtt cct agg ttg aag aga gag ttt gag aaa ggg gaa taa	1293
Lys Asp Val Pro Arg Leu Lys Arg Glu Phe Glu Lys Gly Glu	
420 425 430	

&lt;210&gt; 2

&lt;211&gt; 430

&lt;212&gt; PRT

&lt;213&gt; Campylobacter jejuni

&lt;400&gt; 2

Met Thr Arg Thr Arg Met Glu Asn Glu Leu Ile Val Ser Lys Asn Met	
1 5 10 15	
Gln Asn Ile Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Asn Ile Asn	
20 25 30	
Tyr Lys Arg Leu Pro Arg Glu Tyr Asp Val Phe Arg Cys Asn Gln Phe	
35 40 45	
Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Ile Lys Ala Val Phe	
50 55 60	
Phe Asn Pro Gly Val Phe Leu Gln Gln Tyr His Thr Ala Lys Gln Leu	
65 70 75 80	
Ile Leu Lys Asn Glu Tyr Glu Ile Lys Asn Ile Phe Cys Ser Thr Phe	
85 90 95	
Asn Leu Pro Phe Ile Glu Ser Asn Asp Phe Leu His Gln Phe Tyr Asn	
100 105 110	
Phe Phe Pro Asp Ala Lys Leu Gly Tyr Glu Val Ile Glu Asn Leu Lys	
115 120 125	
Glu Phe Tyr Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr Phe Asn Lys Arg	
130 135 140	

Ile	Thr	Ser	Gly	Val	Tyr	Met	Cys	Ala	Ile	Ala	Ile	Ala	Leu	Gly	Tyr	145	150	155	160
Lys	Thr	Ile	Tyr	Leu	Cys	Gly	Ile	Asp	Phe	Tyr	Glu	Gly	Asp	Val	Ile	165	170		175
Tyr	Pro	Phe	Glu	Ala	Met	Ser	Thr	Asn	Ile	Lys	Thr	Ile	Phe	Pro	Gly	180	185		190
Ile	Lys	Asp	Phe	Lys	Pro	Ser	Asn	Cys	His	Ser	Lys	Glu	Tyr	Asp	Ile	195	200		205
Glu	Ala	Leu	Lys	Leu	Leu	Lys	Ser	Ile	Tyr	Lys	Val	Asn	Ile	Tyr	Ala	210	215		220
Leu	Cys	Asp	Asp	Ser	Ile	Leu	Ala	Asn	His	Phe	Pro	Leu	Ser	Ile	Asn	225	230		235
Ile	Asn	Asn	Asn	Phe	Thr	Leu	Glu	Asn	Lys	His	Asn	Asn	Ser	Ile	Asn	245	250		255
Asp	Ile	Leu	Leu	Thr	Asp	Asn	Thr	Pro	Gly	Val	Ser	Phe	Tyr	Lys	Asn	260	265		270
Gln	Leu	Lys	Ala	Asp	Asn	Lys	Ile	Met	Leu	Asn	Phe	Tyr	Asn	Ile	Leu	275	280		285
His	Ser	Lys	Asp	Asn	Leu	Ile	Lys	Phe	Leu	Asn	Lys	Glu	Ile	Ala	Val	290	295		300
Leu	Lys	Lys	Gln	Thr	Thr	Gln	Arg	Ala	Lys	Ala	Arg	Ile	Gln	Asn	His	305	310		315
Leu	Ser	Tyr	Lys	Leu	Gly	Gln	Ala	Leu	Ile	Ile	Asn	Ser	Lys	Ser	Val	325	330		335
Leu	Gly	Phe	Leu	Ser	Leu	Pro	Phe	Ile	Ile	Leu	Ser	Ile	Val	Ile	Ser	340	345		350
His	Lys	Gln	Glu	Gln	Lys	Ala	Tyr	Lys	Phe	Lys	Val	Lys	Lys	Asn	Pro	355	360		365
Asn	Leu	Ala	Leu	Pro	Pro	Leu	Glu	Thr	Tyr	Pro	Asp	Tyr	Asn	Glu	Ala	370	375		380
Leu	Lys	Glu	Lys	Glu	Cys	Phe	Thr	Tyr	Lys	Leu	Gly	Glu	Glu	Phe	Ile	385	390		395
Lys	Ala	Gly	Lys	Asn	Trp	Tyr	Gly	Glu	Gly	Tyr	Ile	Lys	Phe	Ile	Phe	405	410		415
Lys	Asp	Val	Pro	Arg	Leu	Lys	Arg	Glu	Phe	Glu	Lys	Gly	Glu			420	425		430

&lt;210&gt; 3

&lt;211&gt; 41

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Description of Artificial Sequence:CJ18F 5' primer

<400> 3

cttaggaggt catatgacaa ggactagaat ggaaaatgaa c

41

<210> 4

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:CJ40R 3' primer

<400> 4

cctaggtcga ctcattagtgt gtgatgggtgg tgaatgtccc ctttctcaaa ctctctcttc 60

<210> 5

<211> 231

<212> PRT

<213> Haemophilus influenzae

<220>

<223> Haemophilus influenzae Rd putative open reading  
frame (ORF)

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Met Gln Leu Ile Lys Asn Asn Glu Tyr Glu Tyr Ala Asp Ile Ile Leu  
1 5 10 15

Ser Ser Phe Val Asn Leu Gly Asp Ser Glu Leu Lys Lys Ile Lys Asn  
20 25 30

Val Gln Lys Leu Leu Thr Gln Val Asp Ile Gly His Tyr Tyr Leu Asn  
35 40 45

Lys Leu Pro Ala Phe Asp Ala Tyr Leu Gln Tyr Asn Glu Leu Tyr Glu  
50 55 60

Asn Lys Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Thr Val  
65 70 75 80

Met Gly Tyr Lys Asp Leu Tyr Leu Thr Gly Ile Asp Phe Tyr Gln Glu  
85 90 95

Lys Gly Asn Pro Tyr Ala Phe His His Gln Lys Glu Asn Ile Ile Lys  
100 105 110

Leu Leu Pro Ser Phe Ser Gln Asn Lys Ser Gln Ser Asp Ile His Ser  
115 120 125

Met Glu Tyr Asp Leu Asn Ala Leu Tyr Phe Leu Gln Lys His Tyr Gly  
130 135 140

Val Asn Ile Tyr Cys Ile Ser Pro Glu Ser Pro Leu Cys Asn Tyr Phe  
145 150 155 160

Pro Leu Ser Pro Leu Asn Asn Pro Ile Thr Phe Ile Leu Glu Glu Lys  
165 170 175

Lys Asn Tyr Thr Gln Asp Ile Leu Ile Pro Pro Lys Phe Val Tyr Lys  
                   180                                  185                                  190

Lys Ile Gly Ile Tyr Ser Lys Pro Arg Ile Tyr Gln Asn Leu Ile Phe  
                   195                                  200                                  205

Arg Leu Ile Trp Asp Ile Leu Arg Leu Pro Asn Asp Ile Lys His Ala  
                   210                                  215                                  220

Leu Lys Ser Arg Lys Trp Asp  
   225                                  230

<210> 6  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:6 His tail,  
       (His)6, polyhistidine tag, six adjacent histidines,  
       metal chelate affinity ligand

<400> 6  
 His His His His His His  
       1                                  5

<210> 7  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:linker between  
       two fusion protein domains

<400> 7  
 Gly Gly Gly His  
       1

<210> 8  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:TM-FLAG tag,  
       epitope tag

<400> 8  
 Asp Tyr Lys Asp Asp Asp Asp Lys  
       1                                  5